REMARKS/ARGUMENTS

Claims 1-3, 5-7, 9-10, 12, 22, 37-42, 44-53, 56-57 and 203-204 are currently pending in the application. Claims 4, 8 and 54 have been cancelled without prejudice. Claims 11, 13-21, 23-36, 58-202 and 205-213 have been withdrawn without prejudice because they are drawn to a non-elected invention. Applicants respectfully submit that the foregoing amendments to the claims are supported in the application as originally filed and that no new matter has been added. It is believed that no fees are due at this time. In view of the following remarks and amendments, applicants respectfully request a timely Notice of Allowance be issued in this case.

Claim Rejections under 35 U.S.C. § 112, First Paragraph

Claims 1-3, 5-7, 9-10, 12, 22, 37-42, 44-53, 56-57 and 203-204 were rejected under 35 U.S.C. § 112, first paragraph, for containing subject matter which was not described in the specification to enable one skilled in the art to make and/or use the invention.

The Office asserts that claims 1-3, 5-7, 9-10, 12, 22, 37-42, 44-53, 56-57 and 203-204 are not enabled because neither the prior art nor the specification teaches how to identify the locations of single nucleotide polymorphisms that will likely cause a variation in one or more bases of a nucleic acid sequence. Applicants traverse the rejection.

Applicants respectfully submit that claims 1, 203 and 204, as amended, are enabled by the specification as originally filed. More specifically, the relevant portion of claim 1, as amended, recites:

> identifying the locations of a variation in one or more bases of the nucleic acid sequence where single nucleotide polymorphisms will likely occur based on the assigned variation value.

This step is supported in the specification. (*see e.g.*, paragraphs [0065]-[0067] (page 26, line 22-page 27, line 24)). As a result, Applicants respectfully submit that the application enables claim 1, as amended. Likewise, the relevant portion of claim 203, as amended, recited:

> a code segment for identifying one or more locations that will likely cause a variation in one or more bases of the wild-type gene sequence based on the assigned variation value.

This code segment is supported in the specification. (*see e.g.*, paragraphs [0065]-[0067] (page 26, line 22-page 27, line 24)). As a result, Applicants respectfully submit that the

application enables claim 203, as amended. Similarly, the relevant portion of claim 204, as amended recites:

> a code segment for identifying one or more locations that will likely cause a variation in one or more codons in the wild-type gene sequence based on the assigned variation value.

This code segment is supported in the specification. (*see e.g.*, paragraphs [0065]-[0067] (page 26, line 22-page 27, line 24)). As a result, Applicants respectfully submit that the application enables claim 204, as amended.

The Office also indicated that the specification teaches only comparisons of codons to identify areas of a nucleic acid sequence which may contain SNPs. Applicants respectfully submit that although the examples shown in the specification refer to codons, the methods thought therein are not limited to codons. As shown in Paragraph [0059] (page 21, line 25-page 22, line 9) and Tables 1A and 1B, the changes are only to one base. One skilled in the art would recognize that present invention uses a codon as a group or a frame of reference and that more or less than three bases (codon) could be used. As a result, Applicants respectfully submit that calculating a variation frequency from a first base to a second base is enabled without further clarification. Applicants, however, have amended claims 1 and 203 to reflect the fact that groups of bases or frames of reference are commonly used and such groups are not limited to codons. Specifically, the relevant portion of claim 1, as amended, recites:

> calculating a variation frequency from a first base to a second base within a group of bases in a dataset of two or more genes.

Similarly, the relevant portion of claim 203, as amended, recites:

> a code segment for calculating a variation frequency from a first base to a second base within a group of bases in a nucleic acid dataset

Note that Claim 204 previously recited codons.

For each reason described above, Applicants respectfully submit that the claims are fully enabled because one of skill in the art would understand from the disclosure how to perform the elements recited in claims 1, 203, 204 and the applicable dependent claims without undue experimentation. Accordingly, Applicants request the withdrawal of the rejections and allowance of all pending claims.

Conclusion

Applicants respectfully submit that claims 1-3, 5-7, 9-10, 12, 22, 37-42, 44-53, 56-57 and 203-204, as amended, are fully patentable. Applicants respectfully request that a timely Notice of Allowance be issued in this case. If the examiner has any questions or comments, or if further clarification is required, it is requested that the examiner contact the undersigned at the telephone number listed below.

Respectfully submitted,

CHALKER FLORES, LLP

By _____

Daniel J. Chalker
Reg. No. 40,552
Tel.: (214) 866-0001
Fax: (214) 866-0010

2711 LBJ Frwy
Suite 1036
Dallas, Texas 75234

Date of Transmission: January 19, 2006

I certify that this paper is being transmitted via facsimile to the USPTO at (571) 273-8300 under 37 CFR 1.8 on the date indicated above.

Daniel J. Chalker